

maryh@stic

3148-1

NeWSprinter20

Tue Jul 01 14:59:27 1997 ✓

NeWSprint 2.5 Rev B

Openwin library 3

NeWSprint interpreter 210.0

NeWSprint 2.5

Tue Jul 1 14:57:48 1997

ALIGNMENTS

/organism="Homo sapiens"
 /leiolate="muscular atrophy patient"
 /dev_stage="3 months old"
 /tissue_type="total brain"
 /clone_lib="normalized infant brain cDNA"
 /sex="Female"
 BASE COUNT 78 a 77 c 83 g 62 t
 Query Match 77.8%; Score 14; DB 65; Length 300;
 Best Local Similarity 88.3%; Pred. No. 4.26e-02;
 Matches 16; Conservative 2; Mismatches 2; Indels 0;
 Gaps 0;
 Db 218 gaaggattggcgaccctg 235
 Cp 18 GAAGGATGGCCACCGCTG 1

RESULT 3 LOCUS H7390 448 bp mRNA EST
 DEFINITION yu8e02.r1 Homo sapiens cDNA clone 229370 5'.
 ACCESSION H7390
 NID 91057479
 KEYWORDS SOURCE human clones>229370 primer>M13RPL library=>Soares fetal liver spleen INFLS vector>PT73D (Pharmacia) with a modified polylinker host=>DH10B (ampicillin resistant) Reitel=>Pac I Rait2=>Eco RI Liver and spleen from a 20 week post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo (dt) primer [5', AACCTGGAAAATAATTAAAGCATCTTCTTCTTCTTCTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pcr I and cloned into the Pac I and Eco RI sites of the modified pTR73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M Fatima Bonaldo.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Bumetazoa; Bilateria; Coelomata;
 Denterotomata; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 448)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Riffkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
 Wilson,R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)

Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 332
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.

source 1..448
 /organism="Homo sapiens"
 /clone="229370"
 <1..>448
 mRNA 118 a 93 c 111 g 124 t 2 others
 BASE COUNT
 ORIGIN
 Query Match 77.8%; Score 14; DB 52; Length 448;
 Best Local Similarity 88.9%; Pred. No. 4.26e-02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0;
 Gaps 0;
 Db 58 qaadgatttcgcacccctg 75
 Cp 18 GAAGGATGGCGACGGCTG 1
 RESULT 4 LOCUS W66944 453 bp mRNA
 DEFINITION me29d08.rl Soares mouse embryo NMME13.5 14.5 Mus musculus cDNA
 clone 388911 5' similar to PIR:S44218 S44218 testin - mouse [1].
 ACCESSION W66944
 NID G1375887
 KEYWORDS EST.
 SOURCE Mus musculus
 Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
 Murinae; Mus;
 REFERENCE 1 (bases 1 to 453)
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Scheibenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wyie,T.R., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 TITLE The WashU-HMMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MGI:240743
 Seq primer: mob_REG+ET
 High quality sequence stop: 348.
 Location/Qualifiers
 1..453
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /note="Vector: pTr73D-Pac (Pharmacia) with a modified
 polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5',
 TGTGTACCAATCTGCAACTGGGGCGGCCGAATTTTTTTTTTTTTTTTTTT
 T 3], on equal amounts of mRNA from 2 13.5dpC and 2
 14.5dpC embryos (total RNA provided by Mano Ko, Wayne
 State Univ., from 2). double-stranded cDNA was ligated to

FEATURES source

Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo.
 /clone="38891."
 /clone lib="Soares mouse embryo NME13.5 14.5"
 /sex="Unknown"
 /tissue type="embryo"
 /dev stage="13.5-14.5dpc total fetus"
 /lab host="DH10B"
 <1...>

BASE COUNT
ORIGIN mRNA 111 a 120 c 140 g 82 t

 Query Match Score 14; DB 175; Length 453;
 Best Local Similarity 88.9%; Pred. No. 4.26e-02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 BASE COUNT ORIGIN mRNA 103 a 159 c 162 g 130 t 9 others

 Db 333 qaaggatggtgaccctg 350
 ||||| ||||| ||||| |||||
 Cp 18 GAAGGATGGCCACCTG 1

RESULT 5 LOCUS N95054 563 bp mRNA
 DEFINITION 2b2c05..81 Homo sapiens cDNA clone 305288 3' similar to PIR:SA44218
 ACCESSION N95054
 NID 91267343
 KEYWORDS EST,
 SOURCE human clone=305288 primer=ETPrimer library=Soares parathyroid tumor NBPA vector=pRT3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI Adult.

1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAATGGAGCGCAGCAAAUTTTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Denterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homo.
 REFERENCE 1 (bases 1 to 563)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Riffkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P., and Wilson,R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 WashU-Merck EST Project

Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: esteneration.wustl.edu
 High quality sequence stops: 84
 Source: IMAGE Consortium, LINL.
 This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
 Possible reverse clone: polyT not found.

NCBI gi: 1267343
 FEATURES source
 1..563
 /organism="Homo sapiens"
 /clone=305288
 /note="human"
 <..>563
 BASE COUNT ORIGIN mRNA 103 a 159 c 162 g 130 t 9 others

 Query Match Score 14; DB 211; Length 563;
 Best Local Similarity 88.9%; Pred. No. 4.26e-02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 11 cagggtgcaccatcc 28
 ||||| ||||| ||||| |||||
 Cp 1 CAGCCGTGCCCATCCCTTC 18

 RESULT 6 LOCUS N95054 563 bp mRNA
 DEFINITION 2b2c05..81 Homo sapiens cDNA clone 305288 3' similar to PIR:SA44218
 ACCESSION N95054
 NID 91267343
 KEYWORDS EST,
 SOURCE human clone=305288 primer=ETPrimer library=Soares parathyroid tumor NBPA vector=pRT3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI Adult.
 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAATGGAGCGCAGCAAAUTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH.

ORGANISM Homo sapiens
 Deuterostomia; Chorodata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
 REFERENCE 1 (bases 1 to 563)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Riffkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P., and Wilson,R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 WashU-Merck EST Project

TITLE Wilson,R.
JOURNAL The WashU-Merck EST Project
COMMENT Unpublished (1995)

Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@atson.wustl.edu

HIGH quality sequence stops: 84
 Source: IMAGE Consortium, LILN1
 This clone is available royalty-free through LILN1 ; contact the
 IMAGE Consortium (info@image.liln1.gov) for further information.
 Possible reversed clone: polyT not found.

FEATURES

source	mRNA	103 a	159 c	162 g	130 t	9 others
BASE COUNT						
ORIGIN						

Query Match 77.8%; Score 14; DB 1118; Length 563;
 Best Local Similarity 88.9%; Pred. No. 4.26e-02;
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 11 cagggtgaccatcc 28
 Qy 1 CAGGCTGGCCATCCTTC 18

RESULT AAC05111 638 bp mRNA EST 23-JUL-1996
DEFINITION zhangj10.r1 Soares fetal liver spleen INFSL S1 Homo sapiens cDNA clone 429186 5'.
ACCESSION AAC05111
NID G148900
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 638)
AUTHORS Hillier L., Clark N., Dubucque T., Elliston K., Hawkins M., Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marras M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevastis E., Waterston R., Williamson A., Wohldmann P., and Wilson R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)

Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@atson.wustl.edu

This clone is available royalty-free through LILN1 ; contact the IMAGE Consortium (info@image.liln1.gov) for further information.
 Seq primer: mob: REGA+ET
 High quality sequence stop: 502.
FEATURES

source	mRNA	193 a	175 c	135 g	133 t	2 others
ORIGIN						

Query Match 77.8%; Score 14; DB 121; Length 638;
 Best Local Similarity 88.9%; Pred. No. 4.26e-02;
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 553 caggtgtgcaccaatcc 570
 Qy 1 CAGGGTGCCCCATCCCTTC 18

RESULT R86574 92 bp mRNA EST 02-APR-1996
LOCUS RABEST149M Oryctolagus cuniculus cDNA clone PRABOC149 3'.
DEFINITION
ACCESSION R86574
NID 9947228
KEYWORDS
SOURCE rabbit clone=PRABOC149 primer=M13 forward library=rabbit
 Osteoclast, Dennis Sakai, strain=rabbit2NZ, vector=pSPORT1
REFERENCE host=E. coli DH12S Raftel=SalI Raftc=NotI Poly(A)+ RNA was
 purified from a 97% pure population of osteoclasts prepared from
 the long bones of 10 day old rabbits. First strand cDNA was
 synthesized by priming with an oligo(dT)-NotI anchor-primer and
 second strand cDNA was synthesized by replacement synthesis as
 described by Gubler and Hoffman (Gene 25:283, 1983). Following the
 addition of Sall adaptors and NotI digestion, the cDNA was cloned
 between the Sall (5') and NotI (3') sites of the pSPORT1 (BRL)
ORGANISM Oryctolagus cuniculus
 Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Osteichthyes; Sarcopterygii; Mammalia; Eutheria;
 Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 92)
AUTHORS Sakai,D., Tong,H.-S. and Minkin,C.
TITLE Osteoclast Molecular Phenotyping by Random cDNA Sequencing

JOURNAL	Bone 17 (2), 111-119 (1995)
MEDLINE	96021365
COMMENT	Other ESTs: RABEST149T Contact: Sakai D Basic Sciences University of Southern California USC School of Dentistry, 925 West 34th Street, DEN-4220, Los Angeles, CA 90089-0641 Tel: 213/405563 Fax: 213/407560 Email: sakaimolbio.usc.edu.
FEATURES	Location/Qualifiers
source	1..92 <i>/organism="Oryctolagus cuniculus"</i> <i>/clone="PRABOC149"</i> <i>/strain="New Zealand White"</i>
BASE COUNT	24 a 23 c 21 g 22 t 2 others
ORIGIN	
Query Match	72.2%
Best Local Similarity	88.2%
Matches	<1..>92 15; Conservative
BASE COUNT	24 a 23 c 21 g 22 t 2 others
ORIGIN	
mRNA	Score 13; DB 122; Length 92;
EST	Pred. No. 8.05e-01; 0; Mismatches 2;
Gaps	Indels 0; Gaps
RESULT	9
LOCUS	T93415 241 bp mRNA
DEFINITION	lmeEST0178 LmLV39cDNA Leishmania major cDNA clone Lm244 5' END
ACCESSION	T93415
NID	9726588
KEYWORDS	Db 62 aaggaaaggctcacgtg 78 CP 17 AAGGATGGCGACGCTG 1
ORGANISM	Leishmania major.
SOURCE	Eukaryota; mitochondrial eukaryotes; Euglenozoa; Kinetoplastida; Trypanosomatida; Leishmania.
REFERENCE	Ajioka, J. W. Leishmania major cDNAs Unpublished (1995)
AUTHORS	
TITLE	
JOURNAL	Contact: Ajioka JW Laboratory for Parasite Genome Analysis Cambridge University Department of Pathology, Tennis Court Road, Cambridge CB2 1QE Tel: 01223333923 Fax: 01223333923 Email: jajioka@hmgmp.mrc.ac.uk Seq. primer: T3.
COMMENT	NCBI gi: 726588 Location/Qualifiers 1..241 <i>/organism="Leishmania major"</i> <i>/strain="Lm39"</i> <i>/note="Vector: Lambda UNIZAP; Site_1: NotI; Site_2: EcoRI; Mid or late log promastigotes; Full length: splice 1"</i>
FEATURES	source

oligo used for second strand synthesis, directional cloning NotI at 5' end, XhoI at 3' end.

/clone="Lm244"
 /clone.lib="LmLV39cDNA"
 /lab.host="XL1-Blue MRF".

<1..>241

BASE COUNT	48	a	69	c	64	g	60	t
ORIGIN								
Query Match	72.2%	Score 13;	DB 218;	Length 241;				
Best Local Similarity	100.0%	Pred. No. 8	0.05e-01;					
Matches	13;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps

mRNA

BASE COUNT	48	a	69	c	64	g	60	t
ORIGIN								
Query Match	72.2%	Score 13;	DB 218;	Length 241;				
Best Local Similarity	100.0%	Pred. No. 8	0.05e-01;					
Matches	13;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps

RESULT 10 T93415 241 bp mRNA EST 01-MAY-1996

LOCUS lmEST0178 LmLV39cDNA Leishmania major cDNA clone Lm244 5' END.

DEFINITION T93415

ACCESSION 9726386

NID 9726386

EST.

KEYWORDS

SOURCE Leishmania major.

ORGANISM Leishmania major.

Eukaryota; mitochondrial eukaryotes; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

REFERENCE 1 (bases 1 to 241)

AUTHORS Ajioka, J.W.

TITLE Leishmania major cDNAs

JOURNAL Unpublished (1995)

COMMENT

Contact: Ajioka JW
 Laboratory for Parasite Genome Analysis
 Cambridge University
 Department of Pathology, Tennis Court Road, Cambridge CB2 1QP,
 Tel: 01223333923
 Fax: 01223333923
 Email: ajioka@hgmp.mrc.ac.uk
 Seq primer: T3.

FEATURES source

Location/Qualifiers

1..241
 /organism="Leishmania major"
 /strain="Lm39"
 /note="Vector: Lambda UNIZAP; Site 1: NotI; Site 2: XbaI Mid or late log promastigotes; Full-length; splice leader oligo used for second strand synthesis, directional cloning NotI at 5' end, XhoI at 3' end."
 /clone="Lm244"
 /clone.lib="LmLV39cDNA"
 /lab.host="XL1-Blue MRF".

<1..>241

BASE COUNT	48	a	69	c	64	g	60	t
ORIGIN								
Query Match	72.2%	Score 13;	DB 151;	Length 241;				
Best Local Similarity	100.0%	Pred. No. 8	0.05e-01;					
Matches	13;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps

Db 164 tgccgcatttc 176
Qy 6 TGCCGCATCCTTC 18

RESULT 11 T93466 257 bp mRNA EST 01-MAY-1996

LOCUS T93466 ImLV39cDNA Leishmania major cDNA clone Lm443 5' END.

DEFINITION T93466

ACCESSION 9126639

NID

KEYWORDS EST.

SOURCE Leishmania major.

ORGANISM Trypanosomatidae; Leishmania. Eukaryota; mitochondrial eukaryotes; Euglenozoa; Kinetoplastida; Leishmania major. (bases 1 to 257)

REFERENCE Ajioka, J.W.

AUTHORS

TITLE

JOURNAL Unpublished (1995)

COMMENT Contact: Ajioka JW Laboratory for Parasite Genome Analysis Cambridge University Department of Pathology, Tennis Court Road, Cambridge CB2 1QP, UK. Tel: 01223333923 Fax: 01223333923 Email: jajioka@hmp.mrc.ac.uk Seq primer: T3.

FEATURES

source

Location/Qualifiers

1..257 /organism="Leishmania major"
/strain="Lm443"/>
/not=Vector: Lambda UNIZAP; Site 1: NotI; Site 2: XbaI; Mid or late log promastigotes. Full length : splice leader oligo used for second strand synthesis, directional cloning NotI at 5' end, XbaI at 3' end." /clone lib="ImLV39cDNA"
/clone host="XL1-Blue MRF".

BASE COUNT

ORIGIN

Query Match Score 13; DB 151; Length 265;

Best Local Similarity 100.0%
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 178 tgccgcatttc 190

Query Match Score 13; DB 151; Length 265;

Best Local Similarity 100.0%
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 178 tgccgcatttc 190

Query Match Score 13; DB 151; Length 257;

Best Local Similarity 100.0%
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 178 tgccgcatttc 190

RESULT 12 T93448 265 bp mRNA EST 01-MAY-1996

LOCUS T93448 ImLV39cDNA Leishmania major cDNA clone Lm390 5' END.

DEFINITION T93448

ACCESSION 9726621

NID

KEYWORDS EST.

SOURCE Leishmania major.

ORGANISM Leishmania major. Eukaryota; mitochondrial eukaryotes; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

REFERENCE 1 (bases 1 to 265), Ajioka, J.W.

AUTHORS

TITLE

JOURNAL

COMMENT Contact: Ajioka JW Laboratory for Parasite Genome Analysis Cambridge University Department of Pathology, Tennis Court Road, Cambridge CB2 1QP, UK. Tel: 01223333923 Fax: 01223333923 Email: jajioka@hmp.mrc.ac.uk

Seq primer: T3.

FEATURES	source	NCBI gi: 726621
	Location/Qualifiers	1..265
	/organism="Leishmania major"	
	/strain="LV39"	
	/note="Vector: Lambda UNIZAP; Site 1: NotI; Site 2: XbaI; Mid or late log promastigotes; Full length: splice leader oligo used for second strand synthesis; directional cloning; NotI at 5' end, XbaI at 3' end."	
	/clone="Lm39"	
	/clone lib="LmLV39cdNA"	
	/lab host="XII-Blue MRF", <1..>265	
BASE COUNT	ORIGIN	mRNA 51 a 78 c Query Match 72.2%; Best Local Similarity 100.0%; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	178 tgccgcatttc 190 Qy 6 TGCCGCATCCTTC 18	Score 13; DB 218; Length 265; Pred. No. 8.05e-01; Score 13; DB 64; Length 301; Best Local Similarity 93.3%; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
RESULT	14	LOCUS HSC26F041 301 bp RNA EST 21-SEP-1995 DEFINITION H. sapiens partial cdna sequence; clone c-26f04. ACCESSION F07460 NID 9673120 KEYWORDS partial cdna sequence; transcribed sequence fragment. SOURCE human. ORGANISM Homo sapiens Eukaryota; mitochondrial eukaryotes; Metazoa; Nematoda; Vertebrata; Eutheria; Primates; Catarzhini; Homidae; Homo. Verbrates; Eutheria; Primates; Catarzhini; Homidae; Homo.
REFERENCE	1 (bases 1 to 301)	Genexpress.
AUTHORS		Direct Submission
TITLE		Submitted (19-JAN-1995) Genethon, B.P. 60, 91002 Evry Cedex France and Genetique Moleculaire et Biologie du Developpement, CNRS UPR420 and Genetique Moleculaire et Biologie du Developpement, CNRS UPR420 B.P. 8, 94801 Villejuif Cedex France E-mail: genexpress@genethon.fr
JOURNAL	2 (bases 1 to 301)	Toward an expression map of the <i>C. elegans</i> genome
REFERENCE	2 (bases 1 to 301)	Genexpress.
AUTHORS		The Genexpress cdna program
TITLE		Unpublished (1995) to DDBJ by:
JOURNAL	3 (bases 1 to 301)	Yuki Kohara, Gene Library Lab.
REFERENCE		National Institute of Genetics Deville, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Davignes, M.D., Duprat, S., Houllague R., Jumeau, M.N., Lamy, B., Lorenz, F., Mitchell, R., Marriage-Gamson, R., Pietu, G., Pouillet, Y., Sebastiani-Kabatchi, C. and Tessier, A.
AUTHORS		Phone: 0559-81-6855 Fax : 0559-81-6855 Email:yokohara@ddbj.nig.ac.jp.
TITLE		IMAGE: molecular integration of the analysis of the human genome and its expression
JOURNAL		93277534
MEDLINE		Cloning method: total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector.
COMMENT		Sequencing method: single read, full automatic;

Primer: M13 reverse
cDNA sequence_colinear to mRNA
stretch removed; nothing
Normalization method: Bento Soares, P.N.A.S. 91:9228-9232 (1994);
Genexpress library idt: C;
Genexpress sequence idt: y1c-26f04.
Location/Qualifiers
1..301
/organism="Homo sapiens"
/isolates="muscular atrophy Patient"
/clone lib="normalized infant brain cDNA from B. Soares,
Psychiatry Dept. Columbia University USA."
/sex= female.
/tissue type="total brain"
/dev stage="3 months old"
/base count 48 a 90 c 91 g 71 t 1 others
BASE COUNT
ORIGIN
Query Match 72.2%;
Best Local Similarity 93.3%;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 188 cgtcgccatccatcc 202
|||||||
Qy 4 CGTCCGCCATCCCTTC 18
Query Match 72.2%;
Best Local Similarity 93.3%;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 188 cgtcgccatccatcc 202
|||||||
Qy 4 CGTCCGCCATCCCTTC 18
RESULT 15
LOCUS CEIK127B1R 316 bp mRNA EST 12-DEC-1995
DEFINITION C. elegans cDNA clone yk127b1 : 3' end, single read.
ACCESSION D64881
NID 91117523
EST (expressed sequence tag).
KEYWORDS Caenorhabditis elegans (strain CB1489 him-8(e1489),) (library:
Yuki Kohara unpublished cDNA) Hermaphrodite, male varied whole animal cDNA to mRNA.
ORGANISM Caenorhabditis elegans
Eukaryota; mitochondrial eukaryotes; Metazoa; Nemata; Secernentea; Rhabditida; Rhabditina; Rhabditoidae;
Rhabditidae; Caenorhabditis.
REFERENCE 1 (bases 1 to 316)
AUTHORS Kohara, Y., Motohashi, T., Tabara, H., Sugimoto, A., Watanabe, H., and Nishizaka, A.
TITLE Toward an expression map of the *C. elegans* genome
JOURNAL Unpublished (1995) to DDBJ by:
COMMENT Submitted (23-Aug-1995) to DDBJ by:
Yuki Kohara, Gene Library Lab.
National Institute of Genetics
Yata 1111, Mishima Shizuoka
411 Japan
Phone: 0559-81-6855
Fax : 0559-81-6855
Email:yokohara@ddbj.nig.ac.jp.
FEATURES source
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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 183 aagggtggggcaagc 197
Cp 17 AAGGTGGGCAACC 3

Search completed: Tue Jul 1 13:14:41 1997
Job time : 495 secs.

maryh@stic

3149-1

NeWSprinter20

Tue Jul 01 15:00:23 1997

NeWSprint 2.5 Rev B

Openwin library 3

NeWSprint interpreter 210.0

NeWSprint 2.5

Release 2.1D John F. Collins, Biocomputing Research Unit,
 Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
 Distribution rights by IntelliGenetics, Inc.

n.a. - n.a. database search, using Smith-Waterman algorithm	Tue Jul 1 12:58:46 1997;	MasPar time 37.84 Seconds
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Comp:		GTGCGCACGGGTGAGGAAAG

searched: 333249 seqs, 555961234 bases x 2
post-processing: Minimum Match 0%
Listing first 45 summaries

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16:VRT 17:PLN 18:PRO1 19:PRO2 20:ROD 21:SYN 22:UNC
23:VIR1 24:VIR2

genbank97
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genbank-new1
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113:DNA 114:VRL

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 DEFINITION Frequent incidence of somatic mutations in translocated BCL2 oncogenes of non-Hodgkin's lymphomas
 ACCESSION S72602
 NID 9241046
 KEYWORDS human 697 pre-B cell acute lymphocytic leukemia cell line.
 SOURCE
 ORGANISM Homo sapiens
 Unclassified.
 REFERENCE 1 (bases 1 to 454)
 AUTHORS Tanaka, S., Louie, D.C., Kant, J.A. and Reed, J.C.
 TITLE Oncogenes of non-Hodgkin's lymphomas
 JOURNAL Blood 79 (1), 229-237 (1992)
 MEDLINE 92096610
 REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbleg 72602] from the original journal article. This sequence comes from Fig. 2.

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FEATURES source

CDS

base count

origin

Query Match

Best Local Similarity

Matches

Score

Pred.

No.

Length

Gaps

Indels

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 732
 misc_feature

JOURNAL

MEDLINE

COMMENT

Clean copy sequence for [1] kindly provided by Y.Tsujimoto. The bcl-2 gene is transcribed by alternative splicing into three mRNAs of different sizes. It consists of at least two exons and encodes two proteins which only differ at their carboxy-terminal ends, and it is activated by translocation into proximity with the Ig heavy chain locus. Both the normal and rearranged bcl-2 gene products are expressed in the B-cell leukemia/lymphoma 2 cells. Genomic clone lambda-18-27 contained all the DNA sequences on the 5' of the splice site (position 732).

LOCATION/QUALIFIERS

SOURCE

CDS

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Score

Pred.

No.

Length

Gaps

Indels

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Proc. Natl. Acad. Sci. U.S.A. 83 (14), 5214-5218 (1986)

JOURNAL
 MEDLINE
 COMMENT

Clean copy sequence for [1] kindly provided by Y.Tsujimoto. The bcl-2 gene is transcribed by alternative splicing into three mRNAs of different sizes. It consists of at least two exons and encodes two proteins which only differ at their carboxy-terminal ends, and it is activated by translocation into proximity with the Ig heavy chain locus. Both the normal and rearranged bcl-2 gene products are expressed in the B-cell leukemia/lymphoma 2 cells. Genomic clone lambda-18-27 contained all the DNA sequences on the 5' of the splice site (position 732).

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 732
 misc_feature

/note="alternative splice donor (intron A start)"

BASE COUNT
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ORIGIN
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Query Match
 100.0%; Score 18; DB 75; Length 911;

Best Local Similarity
 100.0%; Score 18; DB 75; Length 911;

Matches
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 18; Conservative
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Db
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RESULT
 3 HUMBCL2A 5086 bp mRNA
 DEFINITION Human B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene mRNA
 ACCESION M13994
 KEYWORDS alternative splicing; bcl-2-alpha protein; proto-oncogene.
 SOURCE Human pre-B-cell leukemia cell line 380, cDNA to mRNA, clones B13.4, 101; and DNA, clone lambda-18-27.
 ORGANISM Homo sapiens
 Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 5086)
 AUTHORS Tsujimoto, Y. and Croce, C.M.
 TITLE Analysis of the structure, transcripts, and protein products of bcl-2, the gene involved in human follicular lymphoma
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 83 (14), 5214-5218 (1986)
 MEDLINE
 86259760

Clean copy sequence for [1] kindly provided by Y.Tsujimoto, 10-FEB-1987.
The bcl-2 gene is transcribed by alternative splicing into three mRNAs of different sizes. It consists of at least two exons and encodes two proteins which only differ at their carboxy-terminal ends, and it is activated by translocation into proximity with the Ig heavy chain locus. Both the normal and rearranged bcl-2 gene products are expressed in the B-cell leukemic lymphoma 2 cells. Genomic clone lambda-18-27 contained all the DNA sequences on the 3' of the splice site (position 2044).
Location/Qualifiers

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ORIGIN	710	bp upstream of Sart 1

RESULT 4 108038 Sequence 1 5105 bp
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 DEFINITION Sequence 1
 ACCESSION 108038
 ID 9389249
 KEYWORDS unknown

ORGANISM	Unknown.
UNCLASSIFIED	Unclassified.
REFERENCE	1 (bases 1 to 5105)
AUTHORS	Tsujiimoto, Y. and Croce, C.M.
TITLE	Diagnostic methods for detecting lymphomas in humans
JOURNAL	Patent : EP 0252685-A2 1 13-JAN-1988;
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Cp	18	GAACGATGGCGAACGCTG	1					
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LOCUS		Rhizobium tropici	nodulation	protein D	(nodD2)	gene, complete cds		
DEFINITION								
ACCESSION	101272							
NID	9152365							
KEYWORDS		nodD gene; nodulation protein D; regulatory protein.						
SOURCE		Rhizobium tropici (strain BR816) DNA.						
ORGANISM		Rhizobium tropici						
EUBACTERIA; Proteobacteria; alpha subdivision; Rhizobium.								
REFERENCE	1	(bases 1 to 1708)						
AUTHORS		van Rijn, P.J.S., Feys, B. and Vanderleyden, J.						
TITLE		Multiple copies of nodD in Rhizobium tropici. CIAT899 and BR816						
JOURNAL		J. Bacteriol. 175, 438-447 (1993)						
MEDLINE								
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Eukaryota; mitochondrial eukaryotes; Mammalia; Eutheria; Primates; Catarrhini; Vertebrata; Eutheria; Primates; Catarrhini.						
REFERENCE	1 (bases 1 to 1846)					
AUTHORS	Seto, M., Jaeger, U., Hockett, R.D., Granit, Goldman, P. and Kormayer, S.J.					
TITLE	Alternative promoters and exons, somatic of the Bcl-2-Ig fusion gene in lymphoma					
JOURNAL	EXPO J. 7 (1), 123-131 (1989)					
MEDLINE	88196071					
FEATURES	Location/Qualifiers					
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Db	882	ggggatggcgacgtcg	899			
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DEFINITION	Borrelia hermsii strain=HS1; ATCC 35209					
ACCESSION	cds_052149					
NID	91654227					
KEYWORDS	.					
ORGANISM	Borrelia hermsii					
Eubacteria; Spirochaetales; Spirochaetidae						
REFERENCE	1 (bases 1 to 1083)					
AUTHORS	Restrepo, B.I., Carter, C.J., Infante, D. et al.					
TITLE	Direct Submission					
JOURNAL	Submitted (22-MAR-1996) Alan G. Barbour 7703 Floyd Curl Drive, San Antonio, TX 78230					
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BASE COUNT	440	a	137	c	270	g	236	t
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Best Local Similarity 100.0%; Pred. No. 9.73⁺⁰; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0;

Db 105 gaagatggcact 119

CP 18 GAAAATGGCCAC 4

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 AC U52149;
 NI 91659227
 DT 01-NOV-1996 (Rel. 49, Created)
 DT 01-NOV-1996 (Rel. 49, Last updated, Version 1)
 DE Borrelia hermsii variable major protein 18 (vmp18) gene, complete cds.
 KW .
 OS Borrelia hermsii
 OC Prokaryota; Bacteria; Gracilicutes; Spirochetes;
 OC Spirochaetales; Spirochaetaceae.
 [1]
 RN 1-1083
 RP Restrepo B.I., Carter C.J., Infante D., Barbour A.G.;
 RT Submitted (22-MAR-1996) to the EMBL/GenBank/DDBJ databases.
 RL Alan G. Barbour, Microbiology, UTHSCSA, 7703 Floyd Curl Drive, San Antonio, TX 78284, USA
 RA Key Location/Qualifiers
 FH source FT
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 FT FT strain="HSI; ATCC 33209"
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Db 105 gaaggatggccacg 119
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RESULT 9 CHRC2A101 29 bp DNA VRT 23-MAY-1996
 DEFINITION Chicken alpha-1 type-II collagen gene; amino acids 578 to 585.
 ACCESSION K02260
 NID 9211336
 KEYWORDS alpha-1 type II collagen; collagen.
 SEGMENT 1 of 6
 SOURCE Gallus gallus (clone: LgCOL(II)) DNA.
 ORGANISM Gallus gallus
 Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Archosauria; Aves; Neognathae; Galliformes;
 Phasianidae; Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 29)
 AUTHORS Sandell,L.J., Yamada,Y., Dorfman,A. and Upholt,W.B.
 TITLE Identification of genomic DNA coding for chicken type II
 procollagen
 JOURNAL J. Biol. Chem. 258 (19), 11617-11621 (1983)
 MEDLINE 84008159
 COMMENT Each procollagen gene codes for the six successive functional
 regions of the protein: signal peptide, NH₂-propeptide, NH-2
 telopeptide, helical peptide, COOH telopeptide, and COOH
 propeptide. The type-II COOH-propeptide is cleaved from the
 procollagen molecule after the triple helical molecule is secreted
 into the extracellular matrix.
 Location/Qualifiers 1..29
 /organism="Gallus gallus"
 /clone="LgCOL(II)."
 /cell_type="reticulocyte"
 <1..24
 /note="prococollagen alpha-1 type-II, AA 578 to 585"
 /codon_start=1
 25..>29
 /note="collagen intron"
 exon 7 a 7 c 11 g 4 t
 Intron Downstream of EcoRI site.

BASE COUNT 91 a 93 c 108 g 72 t
 ORIGIN

FEATURES Source

Query Match 91 a 93 c 108 g 72 t
 Best Local Similarity 77.8%;
 Matches 16; Conservative 16;
 Pred. No. 4.79e+01; Length 364;

Db 265 qaaggatggccacg 282
 Cp 18 GAAGGTGGCCACCGTG 1

RESULT 11 SSPEC60 364 bp RNA
 DEFINITION S_acrofa PEC-60 mRNA.
 ACCESSION X67109
 NID 92033
 KEYWORDS pec-60 gene.

G Query Match 10 S46866 364 bp mRNA
 FT Best Local Similarity 77.8%;
 FT Matches 14; Conservative 0;
 FT Pred. No. 4.79e+01;
 FT Mismatches 0; Indels 0;
 FT Gaps 0;
 FT LOCUS PEC-60=gastrointestinal peptide (swine, duodenum, mRNA, 364 nt).
 FT DEFINITION S46866
 FT ACCESSION 9257597
 FT NID
 FT KEYWORDS swine duodenum.
 FT SOURCE Sus sp.
 FT ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 364)
 AUTHORS Morsaas,M., Cintra,A., Solfrini,V., Ernfors,P., Bortolotti,F.,
 et al.
 Morsaas,M., Cintra,A., Solfrini,V., Ernfors,P., Bortolotti,F.,
 Morrasutti,D.G., Ostenson,C.G., Efendic,S., Agerberth,B., Mutt,V.
 et al.
 Molecular cloning of PEC-60 and expression of its mRNA and peptide
 in the gastrointestinal tract and immune system
 J. Biol. Chem. 267 (28), 19825-19832 (1992);
 93015834
 GenBank staff at the National Library of Medicine created this
 entry (NCBI gibseq 115614) from the original journal article.
 This sequence comes from Fig. 1.
 Location/Qualifiers 1..364
 /organism="Sus sp."
 CDS 23..283
 /note="Gastrointestinal peptide; Author includes
 translated amino acids 5 of putative initiation codon;
 This sequence comes from Fig. 1. Author-given Protein
 sequence is in conflict with the conceptual translation"
 /codon_start=1
 /product="PEC-60"
 /db_xref="PID:9257598"
 /translati on="RQPRPRISMAVRILWVVALALAALFIVDREPVSAEKEQVSFRMPIC
 ERHTEPSDCRUYDPVGTDVTYSECKLCLARIENKQD1QVTRDGC"
 BASE COUNT 91 a 93 c 108 g 72 t
 ORIGIN

Query Match 91 a 93 c 108 g 72 t
 Best Local Similarity 77.8%;
 Matches 16; Conservative 16;
 Pred. No. 4.79e+01; Length 364;

Db 265 qaaggatggccacg 282
 Cp 18 GAAGGTGGCCACCGTG 1

RESULT 11 SSPEC60 364 bp RNA
 DEFINITION S_acrofa PEC-60 mRNA.
 ACCESSION X67109
 NID 92033
 KEYWORDS pec-60 gene.

SOURCE Pig.
 ORGANISM *Sus scrofa*
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Artiodactyla; Suidae; Suina;
 Sub. Metris, M.
 REFERENCE 1 (bases 1 to 364)
 AUTHORS Direct Submission
 JOURNAL Submitted (22-JUN-1992) M. Metris, Dept. of Medical Chemistry, Lab. of Molecular Neurobiology, Karolinska Institute, Box 604 00, 10401 Stockholm, SWEDEN
 FEATURES Location/Qualifiers
 1..364
 /organism="Sus scrofa"
 /clone lib="pig duodenum cDNA library in gt10 4x10 6"
 23..283
 /evidence=experimental
 /coor_start=1
 /product="peptide PEC-60"
 /db_xref="PID:92034"
 /db_xref="SWISS-PROT:P37109"
 /translation="MAVLWVVALALALALFLIVDREVPVSALKQVFSRMAPICEHMTESP
 DCSIYIDPVCGTDGTVSECKLCLARIENKQDICKOGECEC"
 23..76
 /note="peptide PEC-60"
 101..280
 /product="peptide PEC-60"
 mat_peptide 91 a 93 c 108 g 72 t
 BASE COUNT
 ORIGIN Query Match
 Best Local Similarity 77.8%; Score 14; DB 48; Length 364;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 265 gaaggatggcgaatctg 282
 Cp 18 GAAAGATGGGCCACCTG 1
 Query Match
 Best Local Similarity 88.9%; Score 14; DB 48; Length 364;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 265 gaaggatggcgaatctg 282
 Cp 18 GAAAGATGGGCCACCTG 1
 RESULT 12 SPPPRNA 450 bp RNA MAM 06-JUL-1994
 DEFINITION *S.scrofa* mRNA for Platelet basic protein.
 ACCESSION X7935
 NID 9457753
 KEYWORDS platelet basic protein.
 SOURCE Pig.
 ORGANISM Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Artiodactyla; Suidae; Suina;
 Sub. Metris, M.
 REFERENCE 1 (bases 1 to 450)
 AUTHORS Power, C.A., Proudfoot, A.E., Magnenat, E., Bacon, K.B. and Wells, T.N.
 TITLE Molecular cloning and characterisation of a neutrophil chemotactic protein from porcine platelets
 JOURNAL Eur. J. Biochem. 221 (2), 713-719 (1994)
 MEDLINE 94229068
 REFERENCE 2 (bases 1 to 450)
 AUTHORS Power, C.A.
 TITLE Direct Submission
 JOURNAL Submitted (01-MAR-1994) C.A. Power, Glaxo Institute for Molecular Biology, 14 chemin des Aulx, 1228 Plan-les-Ouates, Geneva, SWITZERLAND

SOURCE Pig.
 ORGANISM *Sus scrofa*
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Artiodactyla; Suidae; Suina;
 Sub. Metris, M.
 REFERENCE 1 (bases 1 to 450)
 AUTHORS Direct Submission
 JOURNAL Submitted (22-JUN-1992) M. Metris, Dept. of Medical Chemistry, Lab. of Molecular Neurobiology, Karolinska Institute, Box 604 00, 10401 Stockholm, SWEDEN
 FEATURES Location/Qualifiers
 1..450
 /organism="Sus scrofa"
 /clone lib="lambda zapII porcine platelet cDNA library"
 mRNA
 /product="platelet basic protein"
 <1..450
 /gene="CTAPIII/NAP-2"
 CDS
 91..450
 /gene="CTAPIII/NAP-2"
 /codon_start=1
 /product="platelet basic protein"
 /db_xref="PID:g45754"
 /db_xref="SWISS-PROT:P43030"
 /translation="MSURLGAISSCTTSSPFPVQLVLLPLSLLTLYPATGAAKE
 GRNAHVEURCLCINTVSGIHPNSIQLEVRAGAHCAKVEIAITKNDKICLDPPEA
 RISKIVKOKIMMEDGGSAA"
 mat_peptide 190..447
 /product="CTAPIII/NAP-2"
 /gene="CTAPIII/NAP-2"
 BASE COUNT 110 a 128 c 109 g 103 t
 ORIGIN Query Match
 Best Local Similarity 77.8%; Score 14; DB 48; Length 450;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 224 qaagaatggcgcacgtt 241
 Cp 18 GAAGGATGGCCACGGCTG 1
 RESULT 13 S72412 700 bp mRNA PRI 28-APR-1993
 DEFINITION proteoglycan-large chondroitin sulfate proteoglycan (PCR-1) [monkeys, smooth muscle cells, juvenile aorta, mRNA Partial, 700 nt].
 ACCESSION S72412
 NID 9786543
 KEYWORDS monkeys juvenile aorta smooth muscle cells.
 SOURCE Unknown
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 700)
 AUTHORS Yao, L.Y., Moody, C., Schonherr, E., Wight, T.N. and Sandell, I.J.
 TITLE Identification of the proteoglycan versican in aorta and smooth muscle cells by DNA sequence analysis, in situ hybridization and immunohistochemistry
 Matrix Biol. 14 (3), 213-225 (1994)
 JOURNAL Matrix Biol.
 MEDLINE 95005762
 REMARK GenBank staff at the National Library of Medicine created this entry (NCBI gibbsq 152611) from the original journal article.
 This sequence comes from Fig. 5.
 FEATURES Location/Qualifiers
 1..700
 /organism="Unknown"
 /note="monkey's"
 1..699
 CDS
 /partial
 /note="Description: proteoglycan versican, CSPG; large chondroitin sulfate proteoglycan; mismatch(50[V->A]); This

sequence comes from Fig. 5. Author-given protein sequence is in conflict with the conceptual translation.

/codon_start=1

/product="proteoglycan versican"

/db_xref="PID:978544"

/translation="YPIAPRIVGCGDMMGAKAVRTYGRSPQETYDVYCYVDLHDGD
VFRHITVPSKTFEAAKECENDARLATVGLQAWRNGDQOCYGMWLSASVHPVTV
VARAQGGCILGVFTYFLFENGTPEPDVSFEDACFKERMSDSLVSIGHPIDESESED
EPCESETDEPHDLMAEILPEPPIEIDLYSENEEEECAATDVITPSVQYIN
GKHVTTVPDKPEA."

BASE COUNT 191 a 155 c 192 g 162 t
ORIGIN

Query Match Score 77.8%; Best Local Similarity 93.8%;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Pred. No. 4.79e+01; Pred. Type: conservative

Db 285 cagctgtgcgcacct 300
Qy 1 CAGCTGTGCATCC 16

RESULT 14 RATEBCL2A 1179 bp mRNA ROD 28-NOV-1994
LOCUS Rattus norvegicus bc1-2 mRNA, complete cds.
DEFINITION

ACCESSION L14680
NID 9408946

KEYWORD bc1-2 gene; dinucleotide repeat; oncogene.

SOURCE Rattus norvegicus (library: Clontech; TS95-11-2) brain cDNA to

mRNA.

ORGANISM Rattus norvegicus

Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathii; Myomorpha; Muridae; Murinae; Rattus.

REFERENCE Irie T., Irie S., Krajewski, S. and Reed, J.C.

TITLE Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein

JOURNAL Gene 140 (2), 291-292 (1994)

MEDLINE 94193015

LOCATION/QUALIFIERS

1..1179 /organism="Rattus norvegicus"

/tissue_type="brain".

/tissue_lib="Clontech; TS95-11-2"

235..945

/gene="bcl-2"

/codon_start=1

/db_xref="PID:9408947"

/translation="MAGAGRIVGDNBEIYMKVHKLISORGXEWDTGDEDASPLRAP
TPGFISFOESRTPAVHDTAARTSPLEPLVANGAPALSPVPPVHLTLLRGDFDS
RRYTRDFAEMSSOLHLPFTARGATVVEELFRDGVNNGRTIVAFEGGGMCVGSYN
REMSPIUDNIALMMTEYLNRLHTWIDNGGWDAEVLYGPSMRPLDFSWLSLKILL

repeat_region 1061..1112

/repeat_unit=1061..1062

BASE COUNT_ site 1179 316 c 306 g 262 t
ORIGIN

Query Match Score 77.8%; Best Local Similarity 93.8%;

Pred. No. 4.79e+01; Pred. Type: conservative

Db 1284 97gcgcaccc 1297
Qy 5 GTGCCCATCCTTC 18

Search completed: Tue Jul 1 13:05:12 1997
Job time : 386 secs.

Best Local Similarity 93.8%;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 230 gaaggatggcgcaagc 245
Cp 18 GRAGGATGCCACCC 3

RESULT 15 A19155 1429 bp RNA PAT 09-MAY-1994

LOCUS A19155 DEFINITION ovine IL-1 beta.

ACCESSION A19155
NID 9512009

KEYWORDS Ovis sp..

ORGANISM Ovis sp..

Eukaryote; Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Caprinae; Ovis.

REFERENCE 1 (bases 1 to 1429)

AUTHORS CYTOKINE PRODUCTION

JOURNAL Patent: WO 9203514-A 18-05-MAR-1992;

FEATURES JOURNAL/Qualifiers

source 1..1429

/organism="Ovis sp."

46..846

/codon_start=1

/product="ovine IL-1 beta"

/db_xref="PID:9512010".

/translation="MATVPPFEINEMAYYSDENELLEFVDCPKOMKSTOHLDIGSMC
DGRIQLOIHSQQLNKSERQSVIVAMEKIRSRAYERVPRDDDRSLISLFIPEEPV
FETTSDELICLQAVGQSKCKLQDRBKSLVLDSPCILVKALHLSQNSREVYFCMSPTV
QGERDRNKPVPAVLGIRDKNLWYLSCVKKGDTPTOLEEVDPKVPKRNNEKRVFKYTK
IANTVFEPSVLPNWYLISTSCIEERPVFLGRFRGQDITDFMETLSP".

BASE COUNT 416 a 363 c 315 g 335 t

ORIGIN

Query Match Score 77.8%;

Best Local Similarity 100.0%;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1284 97gcgcaccc 1297
Qy 5 GTGCCCATCCTTC 18

maryh@stic

3147-1

NeWSprinter20

Tue Jul 01 14:58:39 1997

NeWSprint 2.5 Rev B

Openwin library 3

NeWSprint interpreter 210.0

NeWSprint 2.5

PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment of human solid tumors, esp. breast cancer
 PS Example 12; Page 33; 10pp; English.
 CC Antisense oligonucleotides were tested for their ability to induce programmed cell death (DNA fragmentation) in the human lymphoma cell line RS1146. The oligonucleotides are phosphodiesters targeted against the translation initiation site (Q86650-55) or the 5'-cap region (Q86656-58) of a human bcl-2 pre-mRNAs. A bcl-2 sense sequence (Q86659) was used as a control.
 SQ Sequence 20 BP; 4 A; 4 C; 10 G; 2 T;

Query Match 100.0%; Score 18; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.98e-02; i 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 gaaggatggcgacgtg 20
 Cp 18 GAAGGATGGCCACCTG 1

RESULT 2
 ID Q49817 standard; RNA; 22 BP.
 AC Q49817;
 DT 03-MAY-1994 (first entry)
 DE Bcl-2 antisense oligonucleotide.
 KW Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene; expression; myc; ss.
 OS Synthetic.
 PN WO9320200-A.
 PD 14-OCT-1993.
 PF 02-APR-1992; GB-0071275.
 PR 02-APR-1992; GB-0071276.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 PI Evan GI;
 DR WPI; 93-336908/42.

PT Treating tumour cells by de-inhibiting Myc-induced apoptosis - esp. by inhibiting expression of the BCL-2 oncogene e.g. with antisense oligo:nucleotide(s), also increasing survival of cultured cells by expressing BCL-2.
 PT Disclosure; Page 58; 109pp; English.
 CC A DNA construct comprising the bcl-2 coding sequence under control of elements allowing its expression is claimed. Myc-induced cell death can be inhibited in cultured cells by expressing bcl-2.
 CC Myc-induced cell death can be de-inhibited in tumour cells by administration of bcl-2 antisense oligonucleotides.
 SQ Sequence 22 BP; 2 A; 12 C; 4 G; 4 T;

Query Match 100.0%; Score 18; DB 8; Length 22;
 Best Local Similarity 100.0%; Pred. No. 3.38e-02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 cagcgtgcgcaccccttc 20
 Qy 1 CAGCGTGCCCCATCCCTTC 18

RESULT 4
 ID Q86644 standard; DNA; 35 BP.
 AC Q86644;
 DT 27-SEP-1995 (first entry)
 DE Bcl-2 translation initiation region.
 KW Anticode oligomer; antisense oligonucleotide; bcl-2; cancer; therapy; leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease; ss.
 OS Synthetic.
 PN WO9308350-A.
 PD 30-MAR-1995.
 PR 20-SEP-1994; U10725.
 PR 20-SEP-1993; US-124256.
 PA (REED) REED J C.
 PI Reed JC;
 DR WPI; 95-139394/18.
 PT Anti-codon oligomers which bind to bcl-2 mRNA - for the treatment of human solid tumours, esp. breast cancer
 PS The antisense Oligonucleotide TI-AS (Q86643) straddles the translation-initiation site in the mRNA coding strand of the human bcl-2 gene and is complementary to this region. It reduces the expression of bcl-2 gene product thereby inducing programmed cell death of certain cancer cells. The correspond. sense bcl-1 sequence was synthesized for use as a control. Sequence 35 BP; 6 A; 13 G; 8 T;

RESULT 3
 ID Q49816 standard; DNA; 22 BP.
 AC Q49816;

Query Match 100.0%; Score 18; DB 14; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.98e-02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 13 gaagqatggcgacgtctg 30
 Cp 18 GAAGGATGGCGACGCTG 1

RESULT 5
 ID Q49815 standard; DNA; 765 BP.
 AC Q49815;
 DT 03-MAY-1994 (first entry)

DE Bcl-2.
 KW Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;
 KW expression; myc; db.
 OS Homo sapiens.

Location/Qualifiers
 FH Key
 FT CDS
 FT /*tag= a
 FT 31...750

PN W09320200-A.
 PD 14-OCT-1993.
 PF 02-APR-1993; G00686.
 PR 02-APR-1992; GB-0072/75.
 PR 02-APR-1992; GB-0072/76.

PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 PI Evan GI;
 DR 93-316908/42.
 DR P-PSDB; R2312.

PT Treating tumour cells by de-inhibiting Myc-induced apoptosis -
 PT esp. by inhibiting expression of the BCL2 oncogene e.g. with
 PT antisense oligo:nucleotide(s), also increasing survival of
 cultured cells by expressing BCL2.

PS Claim 26; Page 76-77; 109pp; English.
 CC A DNA construct comprising the bcl-2 coding sequence under control
 CC of elements allowing its expression is claimed. Myc-induced cell
 CC death can be inhibited in cultured cells by expressing bcl-2.
 CC Myc-induced cell death can be de-inhibited in tumour cells by admin.
 CC of bcl-2 antisense oligonucleotides.

SQ Sequence 765 BP; 120 A; 251 C; 144 T;

Query Match 100.0%; Score 18; DB 8; Length 765;
 Best Local Similarity 100.0%; Pred. No. 3.98e-02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 26 gaagqatggcgacgtctg 43
 Cp 18 GAAGGATGGCGACGCTG 1

RESULT 6
 ID N81293 standard; DNA; 831 BP.
 AC N81293;
 DT 17-DEC-1990 (first entry)
 DE Sequence of bcl-2 cDNA corresp. to the 3.5 kb transcript encoding
 DE bcl-2-beta
 KW B-cell neoplasm; diagnosis; follicular lymphomas; ss.
 OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS
 FT /*tag= a
 FT EP-232 685-A.
 PN 13-JAN-1988.
 PD 02-JUL-1987; 305863.
 PR 09-JUL-1986; US-883687.
 PA (WIST) Wistar Corp.
 PI Taujimoto Y, Croce CM;
 DR WPI; 88-008633/02.
 DR P-PSDB; P80988.

P-PSDB; P80988.

Detection of B-cell neoplasms -
 PT by extn. of proteins or RNA from B-cells and quantitation using
 PT specific antibody or DNA probe

PS Claim 8; Fig 3; 23pp; English.

CC Human bcl-2 gene substantially free of introns is claimed. Also claimed
 CC is a substantially pure preparation of a protein having an N-terminal
 CC encoded by the first exon of the human bcl-2 gene the protein being
 CC bcl-2-alpha having about 239 (P80988) or 205 (P80988) residues. B-cell
 CC neoplasms which are associated with t(14;18) chromosome translocations
 CC cause an increase in expression of both the mRNA and the protein products
 CC of the bcl-2 gene. This is used to detect B-cell neoplasms including
 CC follicular lymphomas as well as other lymphomas. Bacterial isolates
 CC available as ATCC 67147 and 67148 can be used to express gene prods.
 CC alpha (nB1292) and beta (nB1293) resp. in bacteria.

SQ Sequence 831 BP; 138 A; 254 C; 290 G; 149 T;

Query Match 100.0%; Score 18; DB 1; Length 831;
 Best Local Similarity 100.0%; Pred. No. 3.98e-02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 142 qaaggatggcgacgtctg 159
 Cp 18 GAAGGATGGCGACGCTG 1

RESULT 7
 ID Q86661 standard; DNA; 5086 BP.
 AC Q86661;
 DT 27-SEP-1995 (first entry)
 DE Human bcl-2 gene.
 KW Anticde oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
 KW chemoresistance; ss.

OS Homo sapiens.

PN W09308350-A.
 PD 30-MAR-1995.

PR 20-SEP-1994; 010725.
 PR 20-SEP-1993; US-124256.
 PA (REED) REED J C.

PI Reed JC;
 DR WPI; 95-139394/18.

PT Anti-cde oligomers which bind to bcl-2 mRNA - for the treatment
 PT of human solid tumours esp. breast cancer
 PS Disclosure; Page 65-68; 108pp; English.

CC Reversal of chemoresistance of tumor cells by antisense-mediated
 CC reduction of bcl-2 expression was demonstrated using the
 CC oligonucleotide given in Q86661. This is antisense to the first
 CC 6 codons of the bcl-2 ORF.
 CC Sequence 5086 BP; 1261 A; 1224 C; 1287 G; 1314 T;

Query Match 100.0%; Score 18; DB 14; Length 5086;

Best Local Similarity 100.0%; Pred. No. 3.98e-02; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Standard; cdNA to mRNA; 5086 BP.

Db 1454 gaaggatggcgccacgtg 1471
 Cp 18 GAAGGATGGCCACCTG 1

RESULT 9
 ID N81292 standard; cdNA; 5105 BP.
 AC N81292.
 DT 17-DEC-1990 (first entry)
 DE Sequence of bcl-2 cDNA corresp. to the 5.5 kb transcript encoding
 bcl-2-alpha
 KW B-cell neoplasm; diagnosis; follicular lymphoma; ss.
 OS Homo sapiens.
 FH Key
 FT CDS
 FT /tag= a
 PN EP-254685-A.
 PD 13-JAN-1988.
 PF 02-JUL-1987; 305963.
 PR 09-JUL-1986; DS-883687.
 PA (WIST-) Wistar Corp.
 PI Tsujimoto Y, Croce CM;
 DR WPI; 88-008633/02.
 DR P-PSDB; P80987.

FT Detection of B-cell neoplasms -
 PT by extn. of proteins or RNA from B-cells and quantitation using
 specific antibody or DNA probe

PS Claim 8; Fig 2A-2D; 23BP; English.
 CC A human bcl-2 gene substantially free of introns is claimed. Also claimed
 CC is a substantially pure preparation of a protein having an N-terminal end
 CC encoded by the first exon of the human bcl-2 gene wherein said protein is
 CC bcl-2-alpha having about 239 (P80987) or 205 (P80988) AA residues. B-cell
 CC neoplasms which are associated with t(14;18) chromosome translocations
 CC cause an increase in the expression of both mRNA and the protein prods.
 CC of the bcl-2 gene. This is used to detect B-cell neoplasms including
 CC follicular lymphomas as well as other lymphomas. Bacterial isolates
 CC available as ATCC 67147 and 67148 can be used to express gene prods.
 CC alpha (n81292) and beta (n91293) resp. In bacteria.
 SQ Sequence 5105 BP; 1281 A; 1225 C; 1286 G; 1313 T;

Query Match 100.0%; Score 18; DB 1; Length 5105;
 Best Local Similarity 100.0%; Pred. No. 3.98e-02;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Db 1454 gaaggatggcgccacgtg 1471
 Cp 18 GAAGGATGGCCACCTG 1

RESULT 10
 ID Q51746 standard; cdNA; 91 BP.
 AC Q51746.
 DT 31-MAY-1994 (first entry)
 DE Oligonucleotide probe MK14-A
 KW Oligonucleotide probe MK14-A
 OS Synthetic.
 PN EP-57191-A.
 PD 01-DEC-1993.
 PF 24-MAY-1993; 108325.
 PR 26-MAY-1992; DS-883651.
 PA (BECT) BECTON DICKINSON CO.
 PI Shank DD, Spears PA;
 DR WPI; 93-378844/4B.
 PT New oligo:nucleotide probes specific for Mycobacteria - used for

PCT International Application No. PCT/US01/05333
 Publication No. WO 01/73333
 Publication Date: October 4, 2001
 Priority Date: April 10, 2001
 Title: Detection and amplification of Mycobacteria nucleic acid in samples

Claim 3; Page 14; 23pp; English.

Oligonucleotide probe MK14-A consists of nucleotides 5-95 of CCC
 (Q51745). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51741-59.
 Sequence 91 BP; 5' A; 17 C; 15 G; 4 T;

Query Match	Score 17/	DB 9;	Length 91;
Best Local Similarity	0.4%	Pred. No. 1.66e-01;	
Matches	0;	Mismatches	0;
Matches	0;	Indels	0
Conservative			

Seq 38 **svvvvhvvhvvhvhvhy** 54
 :::::::::::::::::::::
 Dpb 18 **GAGGATGGCCAGGCT** 2

Result 11
 Q51746 standard; cDNA; 91 BP.
 Q51746; AC 31-MAY-1994 (first entry)
 Oligonucleotide probe MK14-A
 Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
 ss. KW Synthetic C.
 DS EP-57191-A.
 ID 01-DIC-1993; 108325.
 ID 24-MAY-1993; 108325.
 ID 26-MAY-1992; US 883651.
 ID (BECT) BECTON DICKINSON CO.

DDB	38	svvvvhhvvvhvvhvhy	54
	18	GAAGGTGGCCACGCT	2
DTP			
RESULT			
ID	Q51746	standard; cDNA; 91 BP.	11
AC	Q51746;		
DT	31-MAY-1994	(first entry)	
DE	Oligonucleotide probe MK14-A		
KW	Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;		
NN	88.		
NN		Synthetic.	
NN		EP-571911-A.	
NN		01-DIC-1993.	
NN		24-MAY-1993; 108325.	
NN		26-MAY-1992; US-883651.	
NN		(BECT) BECTON DICKINSON CO.	

P1 Shank DD, Spears PA;
WPI 93-37884/48.
OR New oligo-nucleotide probes specific for Mycobacteria - used for
detection and amplification of Mycobacteria nucleic acid in
samples

P2 Claim 3: Page 14; 23pp; English.

P3 Oligonucleotide probe M14-A consists of nucleotides 5-95 of MK11
(Q511735). It hybridized to all spp. of mycobacteria tested, but
cross reacted to a few non-mycobacterial spp. The probe may
be useful as an initial screen for mycobacterial infection.
See also Q511735-45 and Q511747-59.

P4 Correspondence: Dr. B. A. T. C., 15 C.
P5 01 Br. 5 17 C. 15 C.

Sequence	31. DR,	J R,	1 / C,	1J G,	4 L;
Query Match	88.9%		Score 16;	DB 9;	
Best Local Similarity	0.0%		Pred. No.	6.766-01;	Length 91;
Matches	0;	Conservative	17;	Mismatches 1;	Indels 0;
				Gaps 0;	
38	svvvvhvvhvvhvhvh	55			
39					
1	CAGCCCTGGCCATGCTTC	18			

RESULT 12
Q22825 standard; DNA: 1429 BP.
Q22825
C 22-JUL-1992 (first entry)
Sequence encoding equine interleukin II-lbeta.
Vaccine; antigen; therapeutic agent; immune response enhancer; -

KW	modulator; ss.
OS	Ovis ammon aries.
FH	46..384
FT	Location/Qualifiers
FT	sig_peptide
FT	/*tag= a
FT	mat_peptide
FT	/*tag= b
FT	misc feature
FT	/*tag= c
FT	label= motif
FT	misc feature
FT	/*tag= d
FT	label= motif
FT	misc feature
FT	/*tag= e
FT	label= motif
FT	misc feature
FT	/*tag= f
FT	label= motif
FT	polyA signal
FT	/*tag= g
PN	WO9203574-A.
PD	05-MAR-1992.
PF	13-AGC-1991; AU0358.
PR	13-AGC-1990; AU-001698.
PR	11-DCC-1990; AU-003859.
PR	15-FEB-1991; AD-004621.
PR	21-JUN-1991; AU-006840.
PA	(YXME-) UNIV MELBOURNE.
PA	(AWOO) AUSTRALIAN WOOL CORP.
PI	Brandon MR, Andrews AE, Nash AD, Neuseen EN;
DR	WPI; 92-096916/12.
DR	P-PSB; R22122.
PT	Nucleotide sequences coding for ruminant cytokine(s) or receptors - used for producing polypeptide(s) for therapeutic and/or adjunct uses in animals
PT	Disclosure; Fig 2A; 93pp; English.
CC	The inventors claim a DNA sequence coding for a polypeptide exhibiting ruminant cytokine or cytochrome receptor activity; ovine interleukine (IL)-1alpha activity; ovine IL-1alpha activity; ovine IL-6 activity; ovine tumour necrosis factor (TNF) alpha activity; ovine IL-2 receptor alpha activity; ovine interferon (IFN)-lambda activity; or ovine IL-2 activity or homologous sequences, derivs. or mutants, or fragments. The recombinant polypeptides are also claimed.
CC	Sequence 1429 BP; 416 A;
SQ	77.8%; Score 14; DB 3; Length 1429;
CC	Best Local Similarity 100.0%; Pred. No. 1.02e+01;
CC	Query Match 335 T;

DE Improved Heat-stable carbamylase gene.
 KW N-carbamoyl-D-alpha-aminoacid; point mutation; random mutation;
 transformant; E.coli; transform; immobilisation; resin; vector; ds.
 OS Agrobacterium radiobacter.

Key
 PH CDS 4..915
 FT /*tag= a
 FT /product= heat_stable_carbamylase
 FT WO9403613-A.
 PN 17-FEB-1994.
 PD 05-AUG-1994; J01101.
 PF 10-AUG-1992; JP-212692.
 PR 21-DEC-1992; JP-340078.
 PA (KANF) KANEGRUCHI KAGAKU KOGYO KK.
 PI Ikenaka Y, Nanba H, Takahashi S, Takano M, Yajima K;
 PI Yamada Y;
 DR WPI; 94-065701/08.
 DR P-PSDB; R46257.
 PT DNA coding for a decarbamylase with improved thermal stability -
 can be used for decarbamylation of
 PT N-carbamoyl-D-alpha-aminoacid(s)
 PS Claim 18; Page 98-100; 177pp; Japanese.
 CC Sequence (Q56983) shows a DNA encoding a thermal stable decarbamylase.
 The enzyme's thermo-stability has been improved by modifying the
 decarbamylase gene using 'point' and 'random' mutations. These are
 shown in sequences (Q56964-92). Sequences (Q56993-96) are also
 improved carbamylases contained within various different vectors for
 transformation.
 Sequence 1559 BP; 321 A; 477 C; 296 T;

Query Match 14; DB 10; Length 1559;
 Best Local Similarity 93.8%;
 Matches 15; Conservative 0; Mismatches 1;
 Indels 0; Gaps 0;

SQ DB 1301 agggaggcgacgtg 1316
 ||||| |||||||
 CP 16 AGGATGGCCACCGCTG 1

RESULT 15
 ID Q56989 standard; DNA; 1559 BP.
 AC Q56989;
 DT 12-AUG-1994 (first entry)
 DE Improved Heat-stable carbamylase gene.
 KW N-carbamoyl-D-alpha-aminoacid; Point mutation; random mutation;
 transformant; E.coli; transform; immobilisation; resin; vector; ds.
 OS Agrobacterium radiobacter.

Key
 PH CDS 4..915
 FT /*tag= a
 FT /product= heat_stable_carbamylase
 FT WO9403613-A.
 PN 17-FEB-1994; J01101.
 PF 05-AUG-1993; JP-212692.
 PR 10-AUG-1992; JP-340078.
 PA (KANF) KANEGRUCHI KAGAKU KOGYO KK.
 PI Ikenaka Y, Nanba H, Takahashi S, Takano M, Yajima K;
 PI Yamada Y;
 DR P-PSDB; R46265.
 PT DNA coding for decarbamylase with improved thermal stability -
 can be used for decarbamylation of
 PT N-carbamoyl-D-alpha-aminoacid(s)
 PS Claim 18; Page 113-115; 177pp; Japanese.
 CC Sequence (Q56963) shows a DNA encoding a thermal stable decarbamylase.
 The enzyme's thermo-stability has been improved by modifying the
 decarbamylase gene using 'point' and 'random' mutations. These are
 shown in sequences (Q56964-92). Sequences (Q56993-96) are also
 improved carbamylases contained within various different vectors for
 transformation.
 Sequence 1559 BP; 323 A; 476 C; 294 T;

Query Match 77.8%; Score 14; DB 10; Length 1559;

Best Local Similarity 93.8%; Pred. No. 1.02e+01;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1301 agaggggcgcacgtg 1316
||| ||||| |||||
Cp 16 AGGATGGCGACGCTG 1

Search completed: Tue Jul 1 13:06:02 1997
Job time : 33 secs.